```
==============================================================
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2008; month=4; day=23; hr=14; min=8; sec=56; ms=527; ]
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Application No: 10620099   Version No: 3.0

                    Input Set:

                    Output Set:

                    Started: 2008-04-09 15:16:12.876
                    Finished: 2008-04-09 15:16:13.531
                    Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 655 ms
            Total Warnings: 21
                Total Errors: 1
    No. of SeqIDs Defined: 23
        Actual SeqID Count: 23

Error code   Error Description

W   213   Artificial or Unknown found in <213> in SEQ ID (3)

W   213   Artificial or Unknown found in <213> in SEQ ID (4)

W   213   Artificial or Unknown found in <213> in SEQ ID (5)

E   257   Invalid sequence data feature in <221> in SEQ ID (5)

W   251   Found intentionally skipped sequence in SEQID (6)

W   251   Found intentionally skipped sequence in SEQID (7)

W   251   Found intentionally skipped sequence in SEQID (8)

W   251   Found intentionally skipped sequence in SEQID (9)

W   251   Found intentionally skipped sequence in SEQID (10)

W   251   Found intentionally skipped sequence in SEQID (11)

W   251   Found intentionally skipped sequence in SEQID (12)

W   251   Found intentionally skipped sequence in SEQID (13)

W   251   Found intentionally skipped sequence in SEQID (14)

W   251   Found intentionally skipped sequence in SEQID (15)

W   251   Found intentionally skipped sequence in SEQID (16)

W   251   Found intentionally skipped sequence in SEQID (17)

W   251   Found intentionally skipped sequence in SEQID (18)

W   251   Found intentionally skipped sequence in SEQID (19)

W   213   Artificial or Unknown found in <213> in SEQ ID (20)

W   213   Artificial or Unknown found in <213> in SEQ ID (21)

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              Input Set:


              Output Set:



                   Started:   2008-04-09 15:16:12.876
                  Finished:   2008-04-09 15:16:13.531
                   Elapsed:   0 hr(s) 0 min(s) 0 sec(s) 655 ms
           Total Warnings:    21
             Total Errors:    1
     No. of SeqIDs Defined:   23
        Actual SeqID Count:   23
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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)

<210> 1
<211> 716
<212> DNA
<213> Aequorea victoria
<400> 1
atgagtaaag gagaagaact tttcactgca gttgtcccaa ttcttgttga attagatggt   60
gatgttaatg gcacaaatt ttctgtcagt ggagagggtg aaggtgatgt aacatacgga   120
aaacttaccc ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt   180
gtcactactt tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg   240
catgactttt tcaagagtgc catgcccgaa ggttatgtac agcaaagaac tatattttc   300
aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga taccctgtt   360
aatagaatcg agttaaaagg tattgatttt aaagaagatg aaacattct ggacataaa   420
ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga   480
atcaaagtta acttcaaaat tagacacaac attgaagatg gaagcgttca actagcagac   540
tattatcaac aaaatactcc aattctcgat ggccctgtcc ttttaccaga caaccattac   600
ctgtccacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt   660
cttgagtttg taacagctgc tgggattaca catggcatgg atgaactata caaata   716

<210> 2
<211> 238
<212> PRT
<213> Aequorea victoria
<400> 2
Met Ser Lys Gly Glu Glu Leu Phe Thr Ala Val Val Pro Ile Leu Val
1   5   10   15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20   25   30
Gly Glu Gly Asp Val Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35   40   45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50   55   60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65   70   75   80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Gln Arg
                85   90   95

```
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175
Gln Leu Ala Asp Tyr Tyr Gln Gln Asn Thr Pro Ile Leu Asp Gly Pro
            180                 185                 190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195                 200                 205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210                 215                 220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                 230                 235

<210> 3
<211> 720
<212> DNA
<213> Artificial sequence
<220>
<223> DNA Sequence encoding engineered Aequorea-related fluorescent
      protein
<400> 3
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac      60
ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac     120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc     180
ctcgtgacca ccttcggcta cggcgtgcag tgcttcgccc gctaccccga ccacatgaag     240
cagcaggact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc     300
ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg     360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggacg acggcaacat cctgggGcac     420
aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac     480
ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagcccgcc     540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac     600
tacctgagct accagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc     660
ctgctggagt tcgtgaccgc cgccgggatc actcacggca tggacgagct gtacaagtaa     720

<210> 4
<211> 239
<212> PRT
<213> Artificial sequence
<220>
<223> Engineered Aequorea-related fluorescent protein
<400> 4
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60
Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

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Gln Gln Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
               100                 105                 110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
           115                 120                 125
Ile Asp Phe Lys Asp Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
       130                 135                 140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
               165                 170                 175
Val Gln Pro Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
           180                 185                 190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
           195                 200                 205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
       210                 215                 220
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                 230                 235


<210> 5
<211> 228
<212> PRT
<213> Artificial sequence

<220>
<223> Engineered Aequorea-related fluorescent protein

<220>
<221>   MOD_RES
<222>   (64)..(66)
<223>   The amide nitrogen of Gly 66 is cyclized onto the amide of Tyr
        65, the amide oxygen of Thr 64 has been removed, and the bond
        between the alpha and beta carbons of Tyr 65 is oxidized to form
        a conjugated GFP chromophore.

<400>   5
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
1                   5                   10                  15
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
               20                  25                  30
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
           35                  40                  45
Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr
       50                  55                  60
Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His
65                  70                  75                  80
Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
                85                  90                  95
Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
               100                 105                 110
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
           115                 120                 125
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
       130                 135                 140
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
```

```
            145                         150                         155                         160
Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
                    165                         170                         175
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
                    180                         185                         190
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
            195                         200                         205
Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
        210                         215                         220
Ala Ala Gly Ile
225


<210> 6
<400> 6
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<210> 7
<400> 7
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<210> 8
<400> 8
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<210> 9
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<210> 10
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<210> 15
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<210> 16
<400> 16
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<210> 17
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<400> 17
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<210> 18
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<210> 19
<400> 19
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<210> 20
<211> 5
<212> PRT
<213> Artificial sequence
<220>
<223> Synthetic localization sequence targeting the nucleus
<400> 20
Lys Lys Lys Arg Lys
1   5

<210> 21
<211> 26
<212> PRT
<213> Artificial sequence
<220>
<223> Synthetic localization sequence targeting the mitochondrion
<400> 21
Met Leu Arg Thr Ser Ser Leu Phe Thr Arg Arg Val Gln Pro Ser Leu
1   5   10   15
Phe Arg Asn Ile Leu Arg Leu Gln Ser Thr
            20   25

<210> 22
<211> 4
<212> PRT
<213> Artificial sequence
<220>
<223> Synthetic localization sequence targeting the endoplasmic
      reticulum
<400> 22
Lys Asp Glu Leu
1

<210> 23
<211> 37
<212> PRT
<213> Artificial sequence
<220>
<223> Synthetic His-tag amino acid sequence
<400> 23
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1   5   10   15
Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20   25   30
Pro Pro Ala Glu Phe
        35